

Amendments to the Specification:

Please cancel the prior abstract and enter in its place the enclosed abstract, which commences on a separate sheet as required by 37 CFR 1.72(b).

Please replace the paragraph at page 3, beginning at line 9 with the following amended paragraph:

The identified NCAM fragment having the sequence EVYVVAENQQGKSKA (FGL peptide; SEQ ID NO:1) involved in the direct interaction between NCAM and FGFR has recently been suggested as a new candidate drug for the treatment of a variety of pathologic disorders where the regulation of activity of FGFR may play the key role (WO 03/016351). WO 03/016351 describes some biological effects of the FGL peptide due to binding and activating FGFR. According to WO 03/016351, presentation of a single copy (monomer) of the peptide to neuronal cells in vitro is enough to promote cell survival and differentiation. However, rather a high concentration of the peptide is needed to achieve the effects.

Please replace the paragraphs at page 26, beginning at line 12 and ending at line 35 with the following amended paragraphs:

A low affinity FGFR binding site of the above molecules is characterised in that it comprises an amino acid sequence which has at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% homology to the sequence EVYVVAENQQGKSKA (SEQ ID NO:1)_{[[,]]}. The sequence EVYVVAENQQGKSKA (SEQ ID NO:1) is derived from the neural cell adhesion molecule (NCAM) and known in the prior art as the FGL peptide of NCAM. The homology of one amino acid sequence with another amino acid sequence is defined as a percentage of identical amino acids in the two collated sequences. The homology between amino acid sequences may be calculated using well known algorithms such as BLOSUM 30, BLOSUM 40, BLOSUM 45, BLOSUM 50, BLOSUM 55, BLOSUM 60, BLOSUM 62, BLOSUM 65, BLOSUM 70, BLOSUM 75, BLOSUM 80, BLOSUM 85, or BLOSUM 90.

In another embodiment, the FGFR binding site of the above molecules comprises an amino acid sequence that has an amino acid sequence having at least 60 %, more preferably at least 70%, more preferably at least 80%, more preferably at least 90%, more preferably 95% positive amino acid matches compared to ~~to~~ the sequence EVYVVAENQQGKSKA (SEQ ID NO:1). Such sequence is defined by the application as a variant of a predetermined sequence, for example SEQ ID NO: 1. A positive amino acid match is defined as an identity or similarity defined by physical and/or chemical properties of the amino acids having the same position in two ~~com-pared~~ compared sequences. Preferred positive amino acid matches of the present invention are K to R, E to D, L to M, Q to E, I to V, I to L, A to S, Y to W, K to Q, S to T, N to S and Q to R.